****
Reviewer Comments:
<210> 15
<211> 3933
<212> DNA
<213> Pseudomonas sp. HJ-2 (phb locus)

<400> 15
gagctcaatg cgcgccagga ctggtgtgcg aggacaaccc ggcgtcaccc ggggacattg
60

ttcacatccg caaagcgcca gagacttgcc cgctgttcca aggtcttaat taacgaggaa
120

tggttaatgg gtactgcgag caatgcggca cgtatagctc tggtcaccgg tggtatgggc
180

ggtatcggta cggcgatcag ccagcgcctg catcgggatg gcttcaccgt ggtggtgggc
240

tgtaatccct actccagccg caaggcttcc tggattgcca cgcaactcga ggcgggcttt
300

cacttccact gcatcgactg cgacatcacc gactgggata gcacccgcca ggccttcgac
360

atggtgcacg agactgtcgg cccgatcgat gtattggtca acaatgccgg catcacccgc
420

gacggcactt tccgcaagat gtccccggaa aactggaagg cggtgatcga taccaatctc
480

accggcctgt tcaacacaac caagcaggtc atcgagggca tgctggccaa gggctgggga
540

cgcgtcatca acatctcctc aatcaatggc cagcgaggcc agttcgggca gaccaactac
600

tccgcggnca aggctggcat tcatggcttc agcatggcct tggcccgcga ggtgagtggc
660

aagggcgtga ccgtcaatac ggtttccccc ggctacatca agaccgacat gaccgcggcg
720

attcgcccgg acatcctcga agacatgatt actggcattc ccgtgggccg tctcggccag
780

cccgaggaga tcgcctcgat cgtggcctgg ctggcctccg atcagtctgc ctatgccacc
840

ggcgccgact tctcggtgaa tggcggcatg aacatgcagt gatgcgccat tcgcgccctc
900

gctcagccat gacatgaggt gttccagatg atcgaagtcg ttatcgtcgc cgccactcgc
960

accgccatcg gcgctttcca ggggagcctg gccggcactc ccgccgttga actgggcgcc
1020

acggtgatcc gccgcctgct cgaacagacc gctctggata gcagtcaggt ggatgaagtg
1080

atactcggcc acgtactcac cgccggtgct ggcagaatac cgctcgccag gcancnggtc
1140

Regarding the above <213> response; per 1.823 of the Sequence Rules, the only valid responses are the Genus species of the organism, "Artificial Sequence", or "Unknown". "Artificial Sequence" and "Unknown" require explanation in the <220>-<223> section; please give the source of the genetic material. Please just list the Genus species as the <213> response; put explanatory matter in the <220>-<223> section; please correct all similar sequences.

The n's at locations 608, 1134, and 1136 are not explained above.

<210> 16
<211> 251
<212> PRT
<213> Pseudomonas sp. HJ-2 (NADPH-dependent acetoacetyl-CoA reductase (phbB))

<400> 16

```
Met Gly Thr Ala Ser Asn Ala Ala Arg Ile Ala Leu Val Thr Gly Gly
  1               5                  10                  15

Met Gly Gly Ile Gly Thr Ala Ile Ser Gln Arg Leu His Arg Asp Gly
             20                  25                  30

Phe Thr Val Val Val Gly Cys Asn Pro Tyr Ser Ser Arg Lys Ala Ser
         35                  40                  45

Trp Ile Ala Thr Gln Leu Glu Ala Gly Phe His Phe His Cys Ile Asp
     50                  55                  60

Cys Asp Ile Thr Asp Trp Asp Ser Thr Arg Gln Ala Phe Asp Met Val
 65                  70                  75                  80

His Glu Thr Val Gly Pro Ile Asp Val Leu Val Asn Asn Ala Gly Ile
                 85                  90                  95

Thr Arg Asp Gly Thr Phe Arg Lys Met Ser Pro Glu Asn Trp Lys Ala
            100                 105                 110

Val Ile Asp Thr Asn Leu Thr Gly Leu Phe Asn Thr Thr Lys Gln Val
        115                 120                 125

Ile Glu Gly Met Leu Ala Lys Gly Trp Gly Arg Val Ile Asn Ile Ser
    130                 135                 140

Ser Ile Asn Gly Gln Arg Gly Gln Phe Gly Gln Thr Asn Tyr Ser Ala
145                 150                 155                 160

Xaa Lys Ala Gly Ile His Gly Phe Ser Met Ala Leu Ala Arg Glu Val
                165                 170                 175
```

Please correct the above <213> response to just indicate the Genus species of the organism; place explanatory matter in the <220>-<223> section. Also, the above <213> response exceeds the Sequence Rules' required 72-character line limit. The "Xaa" at location 161 is not explained above.

<210> 17
<211> 392
<212> PRT
<213> Pseudomonas sp. HJ-2 (beta-ketothiolase (phbA))

<400> 17

```
Met Ile Glu Val Val Ile Val Ala Ala Thr Arg Thr Ala Ile Gly Ala
  1               5                  10                  15

Phe Gln Gly Ser Leu Ala Gly Thr Pro Ala Val Glu Leu Gly Ala Thr
             20                  25                  30

Val Ile Arg Arg Leu Leu Glu Gln Thr Ala Leu Asp Ser Ser Gln Val
         35                  40                  45

Asp Glu Val Ile Leu Gly His Val Leu Thr Ala Gly Ala Gly Arg Ile
     50                  55                  60

Pro Leu Ala Arg Xaa Xaa Val Ile Ala Gly Leu Pro His Ala Val Pro
 65                  70                  75                  80
```

Please correct the above <213> response. Also, the "Xaa's" at locations 69-70 are not explained above.

****

Validated By CRFValidator v 1.0.3

Application No: 10583840 Version No: 2.0

Input Set:

Output Set:

Started: 2009-07-22 14:17:12.979
Finished: 2009-07-22 14:17:15.807
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 828 ms
Total Warnings: 18
Total Errors: 6
No. of SeqIDs Defined: 18
Actual SeqID Count: 18

Error code		Error Description
W	213	Artificial or Unknown found in <213> in SEQ ID (1)
W	213	Artificial or Unknown found in <213> in SEQ ID (2)
W	213	Artificial or Unknown found in <213> in SEQ ID (3)
W	213	Artificial or Unknown found in <213> in SEQ ID (4)
W	213	Artificial or Unknown found in <213> in SEQ ID (5)
W	213	Artificial or Unknown found in <213> in SEQ ID (6)
W	213	Artificial or Unknown found in <213> in SEQ ID (7)
W	213	Artificial or Unknown found in <213> in SEQ ID (8)
W	213	Artificial or Unknown found in <213> in SEQ ID (9)
W	213	Artificial or Unknown found in <213> in SEQ ID (10)
W	213	Artificial or Unknown found in <213> in SEQ ID (11)
W	402	Undefined organism found in <213> in SEQ ID (12)
W	402	Undefined organism found in <213> in SEQ ID (13)
W	402	Undefined organism found in <213> in SEQ ID (14)
W	402	Undefined organism found in <213> in SEQ ID (15)
E	342	'n' position not defined found at POS: 608 SEQID(15)
E	342	'n' position not defined found at POS: 1134 SEQID(15)
E	342	'n' position not defined found at POS: 1136 SEQID(15)
W	402	Undefined organism found in <213> in SEQ ID (16)
E	341	'Xaa' position not defined SEQID (16) POS (161)

Input Set:

Output Set:

Started: 2009-07-22 14:17:12.979
Finished: 2009-07-22 14:17:15.807
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 828 ms
Total Warnings: 18
Total Errors: 6
No. of SeqIDs Defined: 18
Actual SeqID Count: 18

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (17)
E 341	'Xaa' position not defined SEQID (17) POS (69)
E 341	'Xaa' position not defined SEQID (17) POS (70)
W 402	Undefined organism found in <213> in SEQ ID (18)

<110> LG CHEM, LTD.

<120> Poly(3-hydroxyalkanoate) Block Copolymer Having Shape Memory Effect

<130> LC05PCT042

<140> 10583840
<141> 2009-07-22

<150> KR 10-2005-0059907
<151> 2005-07-04

<160> 18

<170> KopatentIn 1.71

<210> 1
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Choi3 (PCR Primer)

<400> 1
ccgccstgsa tcaagtac 18

<210> 2
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Choi4 (PCR Primer)

<400> 2
gytsgtgsyg tcyycgttcc 20

<210> 3
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> HJ-PHB-N (PCR Primer)

<400> 3
caccatgctg agttgcgctc tagc 24

<210> 4

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> HJ-PHB-C (PCR Primer)

<400> 4
tcadmsytty acrtarcgkc ctggygc 27

<210> 5
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> SCL-1 (PCR Primer)

<400> 5
gatcgatacc aatctcaccg 20

<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> SCL-2 (PCR Primer)

<400> 6
caaagccagt ggttcgacgt a 21

<210> 7
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> SCL-3 (PCR Primer)

<400> 7
ctgctgaaac tgttggagc 19

<210> 8
<211> 47
<212> DNA
<213> Artificial Sequence

<220>

<223> SD-BA-N (PCR Primer)

<400> 8
gggggtacca ataaggagat atacatatgg gtactgcgag caatgcg 47

<210> 9
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> BA-C (PCR Primer)

<400> 9
cccactagtt cagcgctcga tggccagc 28

<210> 10
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> SD-phbC-N (PCR Primer)

<400> 10
gggcatatga cccagaagaa caacagcg 28

<210> 11
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> phbC-C (PCR Primer)

<400> 11
cccactagtt cadmscttya crtaacgtcc tggcgcygc 39

<210> 12
<211> 756
<212> DNA
<213> Pseudomonas sp. HJ-2

<220>
<221> variation
<222> (482)
<223> n=A, C, G or T

<400> 12

atgggtactg cgagcaatgc ggcacgtata gctctggtca ccggtggtat gggcggtatc 60

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ccctactcca gccgcaaggc ttcctggatt gccacgcaac tcgaggcggg ctttcacttc 180

cactgcatcg actgcgacat caccgactgg gatagcaccc gccaggcctt cgacatggtg 240

cacgagactg tcggcccgat cgatgtattg gtcaacaatg ccggcatcac ccgcgacggc 300

actttccgca agatgtcccc ggaaaactgg aaggcggtga tcgataccaa tctcaccggc 360

ctgttcaaca caaccaagca ggtcatcgag ggcatgctgg ccaagggctg gggacgcgtc 420

atcaacatct cctcaatcaa tggccagcga ggccagttcg ggcagaccaa ctactccgcg 480

gncaaggctg gcattcatgg cttcagcatg gccttggccc gcgaggtgag tggcaagggc 540

gtgaccgtca atacggtttc ccctggctac atcaagaccg acatgaccgc ggcgattcgc 600

ccggacatcc tcgaagacat gattactggc attcccgtgg gccgtctcgg ccagcccgag 660

gagatcgcct cgatcgtggc ctggctggcc tccgatcagt ctgcctatgc caccggcgcc 720

gacttctcgg tgaatggcgg catgaacatg cagtga 756

<210> 13
<211> 1179
<212> DNA
<213> Pseudomonas sp. HJ-2

<220>
<221> variation
<222> (207)
<223> n=A, C, G or T

<220>
<221> variation
<222> (209)
<223> n=A, C, G or T

<400> 13
atgatcgaag tcgttatcgt cgccgccact cgcaccgcca tcggcgcttt ccaggggagc 60

ctggccggca ctcccgccgt tgaactgggc gccacggtga tccgccgcct gctcgaacag 120

accgctctgg atagcagtca ggtggatgaa gtgatactcg gccacgtact caccgccggt 180

gctggcagaa taccgctcgc caggcancng gtcatcgccg gcctgccaca cgccgtaccg 240

gcgatgaccc tgaacaaggt ctgtggctcc ggcctgaaag ccctgcacct gggcgcccag 300

gccatccgct gtggcgatgc cgaggtggtg attgccggtg gcatggagaa catgagcctg 360

tcgtcctatg tcctgcccaa ggcccgcacc ggcctgcgca tgggccacgc gcagctggtc 420

gacagcatga tcgtcgacgg cctgtgggac gccttcaacg actaccacat ggggatcact 480

gccgagaacc tggtagacaa gtacggcatc agccgcgaag cccaggacga attcgccgcc 540

gcctcgcagc agaaagccgt ggccgccatc gagaccggtc gcttccgcga cgagatcgtc 600

ccggtgagca ttccgcagcg caagggcgag gcgctgagct tcgacaccga cgaacagcca 660

cgcgccggca ccaccgccga gtcgctgggc aagctgaaac cggccttcaa gaacgacggc 720

agcgttactg ccggcaacgc ttccagtctc aacgacggcg ccgccgcggt actgctgatg 780

agtgcggcaa aggccgcagc gcttggtctg ccagtgctgg cgaagatcgc cgcctacgcc 840

aatgccggcg tcgacccggc gatcatgggt atcggaccgg tgtcggccac ccgcagttgc 900

ctggagaagg cgggctggag tctggcagag ctggatctga tcgaggccaa tgaagccttc 960

gcggcccagg ccctggccgt gggtcaggag ctgggctggg atgctggcag ggttaacgtc 1020

aacggcggcg ccatcgccct cggccacccc attggcgcct ccggctgccg cgtactggtc 1080

agcctgctgc atgaaatgct caggcgcgac gcgaaaaaag gcctcgctac cctgtgtatc 1140

ggtggcggcc agggcgtggc gctggccatc gagcgctga 1179

<210> 14
<211> 1701
<212> DNA
<213> Pseudomonas sp. HJ-2 (SCL-PHA synthase (phaC))

<400> 14
atggacaacg gacacacctt tgctcactac tggtcgggtc aggcgccctt catcgccagc 60

ttcgtcctgc agcaactgcg cttatacgtg gcgcaaaata cttggttcag cgggcacgac 120

caaagccagt ggttcgacgt acctgtcgag gcgttggagc aactgcaggc ggactaccaa 180

caacagtggg ccgaacttgg ccagcaattg ctgagctgcc agccgttcgc attcagcgat 240

cgtcgcttcg ccagtggcaa ctggagcgaa ccgctgttcg gttccctggc tgccttctac 300

ctgctgaatt ccggtttcct gctgaaactg ttggagcttc tccccatcga tgagcagaag 360

ccccgccagc gcttgcgtta cttgatcgag caagcgattg ccgcaagcgc cccaagtaac 420

tttctgctga gcaaccctga tgccctgcaa cgcctagtgg aaacccaggg cgccagccta 480

ctaagtggcc tgttgcatct tgccagtgac ctgcaggcag gcaagttgcg ccaatgtgac 540

ttgggcgatt tcgaagtcgg cgtgaatctg gccaccaccc ctggtgccgt ggtactggaa 600

acccctctgt tccagctgat ccagtattcg ccgctcagcg aaacgcaata ccagcggccg 660

atattcatgg tcccgccctg gatcaacaag tactacatcc ttgacctcgg gcccgaaaac 720

tctctaatcc gtcatctact ggagcgaggc catcaagttt ttctgatgtc ctggcgcaac 780

ttcactcagg aacaggccga catcacctgg gagcagatca tccaggacgg agtgatcagc 840

gccctgcgca ctacccgggc catcagtggt gagcgccacc tgaactgttt gggtttctgc 900

atcggcggca ccatgctgag ttgcgctcta gcggtgctgg cagcgcgtgg cgaccaggac 960

attgccagcc tgagtctatt cgccactttt cttgactacc ttgataccgg gccgatcagc 1020

gtcttcgtcg atgagcaact ggtggcctac cgtgagcgca ccatcggtgg ccatggtggc 1080

aaatgtggcc tgttccgcgg tgaggacatg ggcaatacct tctccctgct gcggcccaac 1140

gagctgtggt ggaactacaa cgtagacaaa tatctcaagg ggcagaagcc gctggctctg 1200

ggtctactgt tctggaacaa cgacagcacc aatctgccgg ggcccctgta ttgctggtat 1260

ctgcgccaca cctacctgca gaacgacctc aaatcggggg agttggatct gtgcggcgtc 1320

aagttggatc tgcgggccat agacgcacca gcctacatct tgggaaccca tgacgaccac 1380

atcgtgccct ggcgaagcgc ctatgccagc acggaattgc tgggaggtcc aaagcgcttt 1440

gtcctcggcg cctccggcca catcgccggg gtgatcaacc cgccagatag gaacaagcgc 1500

cattactggg tcaatgaaca catagcgccg gtagctgacg actggctgca gggagctcag 1560

cagcattccg gcagttggtg gggtgactgg ttcgcctggt tgaccggcta tgccggccca 1620

cgcaagcctg ccatcactat gctgggcagt gccgagtacc ccccgcttga acatgcgcca 1680

ggacgttatg tgaagctatg a 1701

<210> 15
<211> 3933
<212> DNA
<213> Pseudomonas sp. HJ-2 (phb locus)

<400> 15
gagctcaatg cgcgccagga ctggtgtgcg aggacaaccc ggcgtcaccc ggggacattg 60

ttcacatccg caaagcgcca gagacttgcc cgctgttcca aggtcttaat taacgaggaa 120

tggttaatgg gtactgcgag caatgcggca cgtatagctc tggtcaccgg tggtatgggc 180

ggtatcggta cggcgatcag ccagcgcctg catcgggatg gcttcaccgt ggtggtgggc 240

tgtaatccct actccagccg caaggcttcc tggattgcca cgcaactcga ggcgggcttt 300

cacttccact gcatcgactg cgacatcacc gactgggata gcacccgcca ggccttcgac 360

atggtgcacg agactgtcgg cccgatcgat gtattggtca acaatgccgg catcacccgc 420

gacggcactt tccgcaagat gtccccggaa aactggaagg cggtgatcga taccaatctc 480

accggcctgt tcaacacaac caagcaggtc atcgagggca tgctggccaa gggctgggga 540

cgcgtcatca acatctcctc aatcaatggc cagcgaggcc agttcgggca gaccaactac 600

tccgcggnca aggctggcat tcatggcttc agcatggcct tggcccgcga ggtgagtggc 660

aagggcgtga ccgtcaatac ggtttccccc ggctacatca agaccgacat gaccgcggcg 720

attcgcccgg acatcctcga agacatgatt actggcattc ccgtgggccg tctcggccag 780

cccgaggaga tcgcctcgat cgtggcctgg ctggcctccg atcagtctgc ctatgccacc 840

ggcgccgact tctcggtgaa tggcggcatg aacatgcagt gatgcgccat tcgcgccctc 900

gctcagccat gacatgaggt gttccagatg atcgaagtcg ttatcgtcgc cgccactcgc 960

accgccatcg gcgctttcca ggggagcctg gccggcactc ccgccgttga actgggcgcc 1020

acggtgatcc gccgcctgct cgaacagacc gctctggata gcagtcaggt ggatgaagtg 1080

atactcggcc acgtactcac cgccggtgct ggcagaatac cgctcgccag gcancnggtc 1140

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ctgaaagccc tgcacctggg cgcccaggcc atccgctgtg gcgatgccga ggtggtgatt 1260

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ttcaacgact accacatggg gatcactgcc gagaacctgg tagacaagta cggcatcagc 1440

cgcgaagccc aggacgaatt cgccgccgcc tcgcagcaga aagccgtggc cgccatcgag 1500

accggtcgct tccgcgacga gatcgtcccg gtgagcattc cgcagcgcaa gggcgaggcg 1560

ctgagcttcg acaccgacga acagccacgc gccggcacca ccgccgagtc gctgggcaag 1620

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gacggcgccg ccgcggtact gctgatgagt gcggcaaagg ccgcagcgct tggtctgcca 1740

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cgctgagtga cgctttcgcg actctgccgg acgtgccccc ctgcacccgc accgccaggc 2160

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ttcatcgcca gcttcgtcct gcagcaactg cgcttatacg tggcgcaaaa tacttggttc 2340

agcgggcacg accaaagcca gtggttcgac gtacctgtcg aggcgttgga gcaactgcag 2400

gcggactacc aacaacagtg ggccgaactt ggccagcaat tgctgagctg ccagccgttc 2460

gcattcagcg atcgtcgctt cgccagtggc aactggagcg aaccgctgtt cggttccctg 2520

gctgccttct acctgctgaa ttccggtttc ctgctgaaac tgttggagct tctccccatc 2580

gatgagcaga agccccgcca gcgcttgcgt tacttgatcg agcaagcgat tgccgcaagc 2640

gccccaagta actttctgct gagcaaccct gatgccctgc aacgcctagt ggaaacccag 2700

ggcgccagcc tactaagtgg cctgttgcat cttgccagtg acctgcaggc aggcaagttg 2760

cgccaatgtg acttgggcga tttcgaagtc ggcgtgaatc tggccaccac ccctggtgcc 2820

gtggtactgg aaaccccctct gttccagctg atccagtatt cgccgctcag cgaaacgcaa 2880

taccagcggc cgatattcat ggtcccgccc tggatcaaca agtactacat ccttgacctc 2940

gggcccgaaa actctctaat ccgtcatcta ctggagcgag gccatcaagt ttttctgatg 3000

tcctggcgca acttcactca ggaacaggcc gacatcacct gggagcagat catccaggac 3060

ggagtgatca gcgccctgcg cactacccgg gccatcagtg gtgagcgcca cctgaactgt 3120

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ggcgaccagg acattgccag cctgagtcta ttcgccactt ttcttgacta ccttgatacc 3240

gggccgatca gcgtcttcgt cgatgagcaa ctggtggcct accgtgagcg caccatcggt 3300

ggccatggtg gcaaatgtgg cctgttccgc ggtgaggaca tgggcaatac cttctccctg 3360

ctgcggccca acgagctgtg gtggaactac aacgtagaca aatatctcaa ggggcagaag 3420

ccgctggctc tgggtctact gttctggaac aacgacagca ccaatctgcc ggggcccctg 3480

tattgctggt atctgcgcca cacctacctg cagaacgacc tcaaatcggg ggagttggat 3540

ctgtgcggcg tcaagttgga tctgcgggcc atagacgcac cagcctacat cttgggaacc 3600

catgacgacc acatcgtgcc ctggcgaagc gcctatgcca gcacggaatt gctgggaggt 3660

ccaaagcgct ttgtcctcgg cgcctccggc cacatcgccg gggtgatcaa cccgccagat 3720

aggaacaagc gccattactg ggtcaatgaa cacatagcgc cggtagctga cgactggctg 3780

cagggagctc agcagcattc cggcagttgg tggggtgact ggttcgcctg gttgaccggc 3840

tatgccggcc cacgcaagcc tgccatcact atgctgggca gtgccgagta ccccccgctt 3900

gaacatgcgc caggacgtta tgtgaagcta tga 3933

<210> 16
<211> 251
<212> PRT
<213> Pseudomonas sp. HJ-2 (NADPH-dependent acetoacetyl-CoA reductase (phbB))

<400> 16
Met Gly Thr Ala Ser Asn Ala Ala Arg Ile Ala Leu Val Thr Gly Gly
1 5 10 15

Met Gly Gly Ile Gly Thr Ala Ile Ser Gln Arg Leu His Arg Asp Gly
20 25 30

Phe Thr Val Val Val Gly Cys Asn Pro Tyr Ser Ser Arg Lys Ala Ser
35 40 45

Trp Ile Ala Thr Gln Leu Glu Ala Gly Phe His Phe His Cys Ile Asp
50 55 60

Cys Asp Ile Thr Asp Trp Asp Ser Thr Arg Gln Ala Phe Asp Met Val
65 70 75 80

His Glu Thr Val Gly Pro Ile Asp Val Leu Val Asn Asn Ala Gly Ile
85 90 95

Thr Arg Asp Gly Thr Phe Arg Lys Met Ser Pro Glu Asn Trp Lys Ala
100 105 110

Val Ile Asp Thr Asn Leu Thr Gly Leu Phe Asn Thr Thr Lys Gln Val
115 120 125

Ile Glu Gly Met Leu Ala Lys Gly Trp Gly Arg Val Ile Asn Ile Ser
130 135 140

Ser Ile Asn Gly Gln Arg Gly Gln Phe Gly Gln Thr Asn Tyr Ser Ala
145 150 155 160

Xaa Lys Ala Gly Ile His Gly Phe Ser Met Ala Leu Ala Arg Glu Val
165 170 175

Ser Gly Lys Gly Val Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Lys
180 185 190

Thr Asp Met Thr Ala Ala Ile Arg Pro Asp Ile Leu Glu Asp Met Ile
195 200 205

Thr Gly Ile Pro Val Gly Arg Leu Gly Gln Pro Glu Glu Ile Ala Ser
210 215 220

Ile Val Ala Trp Leu Ala Ser Asp Gln Ser Ala Tyr Ala Thr Gly Ala
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Asp Phe Ser Val Asn Gly Gly Met Asn Met Gln
245 250

<210> 17
<211> 392
<212> PRT
<213> Pseudomonas sp. HJ-2 (beta-ketothiolase (phbA))

<400> 17

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Phe Gln Gly Ser Leu Ala Gly Thr Pro Ala Val Glu Leu Gly Ala Thr
             20                  25                  30

Val Ile Arg Arg Leu Leu Glu Gln Thr Ala Leu Asp Ser Ser Gln Val
         35                  40                  45

Asp Glu Val Ile Leu Gly His Val Leu Thr Ala Gly Ala Gly Arg Ile
     50                  55                  60

Pro Leu Ala Arg Xaa Xaa Val Ile Ala Gly Leu Pro His Ala Val Pro
 65                  70                  75                  80

Ala Met Thr Leu Asn Lys Val Cys Gly Ser Gly Leu Lys Ala Leu His
                 85                  90                  95

Leu Gly Ala Gln Ala Ile Arg Cys Gly Asp Ala Glu Val Val Ile Ala
            100                 105                 110

Gly Gly Met Glu Asn Met Ser Leu Ser Ser Tyr Val Leu Pro Lys Ala
        115                 120                 125

Arg Thr Gly Leu Arg Met Gly His Ala Gln Leu Val Asp Ser Met Ile
    130                 135                 140

Val Asp Gly Leu Trp Asp Ala Phe Asn Asp Tyr His Met Gly Ile Thr
145                 150                 155                 160

Ala Glu Asn Leu Val Asp Lys Tyr Gly Ile Ser Arg Glu Ala Gln Asp
                165                 170                 175

Glu Phe Ala Ala Ala Ser Gln Gln Lys Ala Val Ala Ala Ile Glu Thr
            180                 185                 190

Gly Arg Phe Arg Asp Glu Ile Val Pro Val Ser Ile Pro Gln Arg Lys
        195                 200                 205

Gly Glu Ala Leu Ser Phe Asp Thr Asp Glu Gln Pro Arg Ala Gly Thr
    210                 215                 220

Thr Ala Glu Ser Leu Gly Lys Leu Lys Pro Ala Phe Lys Asn Asp Gly
225                 230                 235                 240

Ser Val Thr Ala Gly Asn Ala Ser Ser Leu Asn Asp Gly Ala Ala Ala
                245                 250                 255

Val Leu Leu Met Ser Ala Ala Lys Ala Ala Ala Leu Gly Leu Pro Val
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